Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (currently amended) A computer-implemented method for analyzing a plurality of transcript sequences in a cluster comprising:

aligning the transcript sequences in the cluster with their corresponding genomic sequences;

determining the quality of the cluster according to the alignment; and

modifying the cluster according to the determined quality to improve alignment quality.

2. (currently amended) The method of Claim 1 wherein the step of determining further comprises classifying a cluster as a chimeric cluster if the cluster is aligned to two separate locations in the genomic sequence.

3. (original) The method of Claim 2 wherein the chimeric cluster has at least 5% of its sequences aligned to each of the two separate locations.

4. (original) The method of Claim 3 wherein the chimeric cluster has at least 10% of its sequences aligned to each of the two separate locations.

5. (original) The method of Claim 4 wherein the chimeric cluster has at least 20% of its sequences aligned to each of the two separate locations.

6. (original) The method of Claim 5 wherein the chimeric cluster has at least 30% of its sequences aligned to each of the two separate locations.

7. (currently amended) The method of Claims 3, 4, ~~or~~ 5, or 6 further comprising subclustering the chimeric clusters; realigning subclusters' sequences to the genomic sequence; and analyzing the re-aligning to determine chimeric clusters.

8. (original) The method of Claim 7 wherein the process is repeated until no chimeric cluster is detected.

9. (currently amended) The method of Claim 1 wherein the step of determining comprises detecting clusters with consensus sequences which overlap in genomic space.

10. (currently amended) The method of Claim 9 further comprising merging the clusters with consensus sequences which overlap in genomic space.

11. (currently amended) The method of Claim 1 wherein the step of determining comprises detecting clusters with consensus sequences within 1000 bases and on the same strand.

12. (currently amended) The method of Claim 11 further comprising merging the clusters with consensus sequences within 1000 bases and on the same strand.

13. (withdrawn) A method for triming a transcript sequence comprising: aligning the transcript sequence to its corresponding genomic sequence; removing a side sequence of the transcript sequence if the side is poorly aligned with the genomic sequence.

14. (withdrawn) The method of Claim 13 wherein the transcript sequence aligns with the genomic sequence with at least 80% identity.

15. (withdrawn) The method of Claim 14 wherein the transcript sequence aligns with the genomic sequence with at least 90% identity.

16. (currently amended) A computer-implemented method of designing a nucleic acid probe array comprising:

aligning a plurality of transcript sequences in a cluster to their corresponding genomic sequence;

modifying the clusters ~~according to their aligning~~ that are not optimally aligned to the genomic sequence to obtain at least one modified cluster wherein the modified cluster display an improved alignment to said genomic sequence; and

selecting probes targeting the at least one modified cluster to design the nucleic acid probe array.

17. (previously amended) The method of Claim 16 wherein the step of modifying comprises subclustering chimeric clusters wherein a cluster is classified as a chimeric cluster if the cluster is aligned to two separate locations in the genomic sequence.

18. (canceled)

19. (previously amended) The method of Claim 17 wherein the chimeric cluster has at least 5% of its sequences aligned to each of the two separate locations.

20. (original) The method of Claim 19 wherein the chimeric cluster has at least 10% of its sequences aligned to each of the two separate locations.

21. (original) The method of Claim 20 wherein the chimeric cluster has at least 20% of its sequences aligned to each of the two separate locations.

22. (original) The method of Claim 21 wherein the chimeric cluster has at least 30% of its sequences aligned to each of the two separate locations.

23. (original) The method of Claim 16 wherein the step of modifying comprises merging the clusters with consensus which overlap in genomic space.

24. (original) The method of Claims 16 further comprising merging the clusters with consensus within 1000 bases and on the same strand.

25. (withdrawn) A method of designing a nucleic acid probe array comprising:

aligning a transcript sequence to its corresponding genomic sequence;

triming a side of the transcript sequence to obtain a trimmed transcript sequence if the side of the transcript sequence is poorly align with the genomic sequence; and

selecting probes targeting the trimmed transcript sequence or clusters including the trimmed transcript sequence.

26. (currently amended) A computer readable medium comprising computer-executable instructions for performing the method of analyzing a plurality of transcript sequences in a cluster comprising:

aligning transcript sequences from the cluster with genomic sequences;

determining the quality of the cluster according to the alignment; and

modifying the cluster according to the determined quality to improve alignment quality.

27. (currently amended) The computer readable medium of Claim 26 wherein the step of determining further comprises classifying a cluster as a chimeric cluster if the cluster is aligned to two separate locations in the genomic sequence.

28. (original) The computer readable medium of Claim 27 wherein the chimeric cluster has at least 5% of its sequences aligned to each of the two separate locations.

29. (original) The computer readable medium of Claim 28 wherein the chimeric cluster has at least 10% of its sequences aligned to each of the two separate locations.

30. (original) The computer readable medium of Claim 29 wherein the chimeric cluster has at least 20% of its sequences aligned to each of the two separate locations.

31. (original) The computer readable medium of Claim 30 wherein the chimeric cluster has at least 30% of its sequences aligned to each of the two separate locations.

32. (currently amended) The computer readable medium of Claims 28, 29, 30 or 31 further comprising subclustering the chimeric clusters; realigning subclusters' sequences to the genomic sequence; and analyzing the re-aligning to determine chimeric clusters.

33. (original) The computer readable medium of Claim 32 wherein the process is repeated until no chimeric cluster is detected.

34. (currently amended) The computer readable medium of Claim 33 wherein the step of determining comprises detecting clusters with a consensus sequence that overlaps in the genomic space.

35. (currently amended) The computer readable medium of Claim 34 further comprising merging the clusters with consensus sequences which overlap in genomic space.

36. (currently amended) The computer readable medium of Claim 35 wherein the step of determining comprises detecting clusters with consensus sequences within 1000 bases and on the same strand.

37. (currently amended) The computer readable medium of Claim 36 further comprising merging the clusters with consensus sequences within 1000 bases and on the same strand.

38. (withdrawn) A computer readable medium comprising computer-executable instructions for performing the method comprising: aligning a transcript sequence to its corresponding genomic sequence; removing a side sequence of the transcript sequence if the side is poorly aligned with the genomic sequence.

39. (withdrawn) The computer readable medium of Claim 38 wherein the transcript sequence aligns with the genomic sequence with at least 80% identity.

40. (withdrawn) The computer readable medium of Claim 39 wherein the transcript sequence aligns with the genomic sequence with at least 90% identity.

41. (currently amended) A computer readable medium comprising computer-executable instructions for performing the method of designing a nucleic acid probe array comprising:

aligning a plurality of transcript sequences in a cluster to their corresponding genomic sequence;

modifying the clusters ~~according to their aligning~~ that are not optimally aligned to the genomic sequence to obtain at least one modified cluster wherein the modified cluster display an improved alignment to said genomic sequence; and

selecting probes targeting the at least one modified cluster to design the nucleic acid probe array.

42. (previously amended) The computer readable medium of Claim 41 wherein the step of modifying comprises subclustering a chimeric cluster wherein a cluster is

classified as a chimeric cluster if the cluster is aligned to two separate locations in the genomic sequence.

43. (canceled)

44. (previously amended) The computer readable medium of Claim 42 wherein the chimeric cluster has at least 5% of its sequences aligned to each of the two separate locations.

45. (original) The computer readable medium of Claim 44 wherein the chimeric cluster has at least 10% of its sequences aligned to each of the two separate locations.

46. (original) The computer readable medium of Claim 45 wherein the chimeric cluster has at least 20% of its sequences aligned to each of the two separate locations.

47. (original) The computer readable medium of Claim 46 wherein the chimeric cluster has at least 30% of its sequences aligned to each of the two separate locations.

48. (currently amended) The computer readable medium of Claim 47 wherein the step of modifying comprises merging the clusters with consensus sequences which overlap in genomic space.

49. (currently amended) The computer readable medium of Claims 48 further comprising merging the clusters with consensus sequences within 1000 bases and on the same strand.

50. (withdrawn) A computer readable medium comprising computer-executable instructions for performing the method of

aligning a transcript sequence to its corresponding genomic sequence;

trimming a side of the transcript sequence to obtain a trimmed transcript sequence if the side of the transcript sequence is poorly align with the genomic sequence; and

selecting probes targeting the trimmed transcript sequence or clusters including the trimmed transcript sequence.